

SEQUENCE LISTING

<110> Valenzuela et al.

<120> DORSAL TISSUE AFFECTING FACTOR AND COMPOSITIONS

<130> REG132-B1

<140> Not Yet Known

<141> Filed Herewith

<150> 09/167,874

<151> 1998-10-07

<150> 08/485,721

<151> 1995-07-06

<150> 08/392,935

<151> 1995-09-22

<150> PCT/US93/08326

<151> 1993-09-02

<150> 07/957,401

<151> 1992-10-06

<150> 07/950,410

<151> 1992-09-23

<150> 07/939,954

<151> 1992-09-03

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(696)

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Met	Glu	Arg	Cys	Pro	Ser	Leu	Gly	Val	Thr	Leu	Tyr	Ala	Leu	Val	Val	
1				5				10					15			

gtc	ctg	ggg	ctg	cgg	gcg	aca	ccg	gcc	ggc	ggc	cag	cac	tat	ctc	cac	96
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Val	Leu	Gly	Leu	Arg	Ala	Thr	Pro	Ala	Gly	Gly	Gln	His	Tyr	Leu	His	
			20					25					30			
atc	cgc	ccg	gca	ccc	agc	gac	aac	ctg	ccc	ctg	gtg	gac	ctc	atc	gaa	144
Ile	Arg	Pro	Ala	Pro	Ser	Asp	Asn	Leu	Pro	Leu	Val	Asp	Leu	Ile	Glu	
		35					40				45					
cac	cca	gac	cct	atc	ttt	gac	ccc	aag	gaa	aag	gat	ctg	aac	gag	acg	192
His	Pro	Asp	Pro	Ile	Phe	Asp	Pro	Lys	Glu	Lys	Asp	Leu	Asn	Glu	Thr	
		50				55					60					
ctg	ctg	cgc	tcg	ctg	ctc	ggg	ggc	cac	tac	gac	cca	ggc	ttc	atg	gcc	240
Leu	Leu	Arg	Ser	Leu	Leu	Gly	Gly	His	Tyr	Asp	Pro	Gly	Phe	Met	Ala	
	65					70				75					80	
acc	tcg	ccc	ccc	gag	gac	cgg	ccc	ggc	ggg	ggc	ggg	ggt	gca	gct	ggg	288
Thr	Ser	Pro	Pro	Glu	Asp	Arg	Pro	Gly	Gly	Gly	Gly	Gly	Ala	Ala	Gly	
				85				90						95		
ggc	gcg	gag	gac	ctg	gcg	gag	ctg	gac	cag	ctg	ctg	cgg	cag	cgg	ccg	336
Gly	Ala	Glu	Asp	Leu	Ala	Glu	Leu	Asp	Gln	Leu	Leu	Arg	Gln	Arg	Pro	
			100					105					110			
tcg	ggg	gcc	atg	ccg	agc	gag	atc	aaa	ggg	cta	gag	ttc	tcc	gag	ggc	384
Ser	Gly	Ala	Met	Pro	Ser	Glu	Ile	Lys	Gly	Leu	Glu	Phe	Ser	Glu	Gly	
		115					120					125				
ttg	gcc	cag	ggc	aag	aag	cag	cgc	cta	agc	aag	aag	ctg	cgg	agg	aag	432
Leu	Ala	Gln	Gly	Lys	Lys	Gln	Arg	Leu	Ser	Lys	Lys	Leu	Arg	Arg	Lys	
		130				135					140					
tta	cag	atg	tgg	ctg	tgg	tcg	cag	aca	ttc	tgc	ccc	gtg	ctg	tac	gcg	480
Leu	Gln	Met	Trp	Leu	Trp	Ser	Gln	Thr	Phe	Cys	Pro	Val	Leu	Tyr	Ala	
	145					150				155					160	
tgg	aac	gac	ctg	ggc	agc	cgc	ttt	tgg	ccg	cgc	tac	gtg	aag	gtg	ggc	528
Trp	Asn	Asp	Leu	Gly	Ser	Arg	Phe	Trp	Pro	Arg	Tyr	Val	Lys	Val	Gly	
			165					170					175			
agc	tgc	ttc	agt	aag	cgc	tcg	tgc	tcc	gtg	ccc	gag	ggc	atg	gtg	tgc	576
Ser	Cys	Phe	Ser	Lys	Arg	Ser	Cys	Ser	Val	Pro	Glu	Gly	Met	Val	Cys	
		180						185					190			
aag	ccg	tcc	aag	tcc	gtg	cac	ctc	acg	gtg	ctg	cgg	tgg	cgc	tgt	cag	624
Lys	Pro	Ser	Lys	Ser	Val	His	Leu	Thr	Val	Leu	Arg	Trp	Arg	Cys	Gln	
		195					200					205				
cgg	cgc	ggg	ggc	cag	cgc	tgc	ggc	tgg	att	ccc	atc	cag	tac	ccc	atc	672

Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
 210 215 220

att tcc gag tgc aag tgc tgc tag
 Ile Ser Glu Cys Lys Cys Ser Cys
 225 230

699

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 35 40 45

His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
 50 55 60

Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
 65 70 75 80

Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Ala Ala Gly
 85 90 95

Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
 100 105 110

Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
 115 120 125

Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
 130 135 140

Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
 145 150 155 160

Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
 165 170 175

Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys

180

185

190

Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
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Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
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Ile Ser Glu Cys Lys Cys Ser Cys
 225 230

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<210> 4

<211> 12

<212> PRT

<213> frog and mouse

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Arg Phe Trp Pro Arg Tyr Val Lys Val Gly Ser Cys
 1 5 10

<210> 5

<211> 14

<212> PRT

<213> frog and mouse

<400> 5

Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys Lys
 1 5 10

<210> 6

<211> 8

<212> PRT

<213> frog and mouse

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Leu Arg Trp Arg Cys Gln Arg Arg
1 5

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Ile Ser Glu Cys Lys Cys Ser Cys
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<212> DNA
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<210> 9
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<220>
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<210> 10
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<222> (421)..(1116)

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 <222> (235)
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tcgaaattaa ccctcactaa agggaacaaa agctggagct ccaccgcggt ggcgggccgcc 180

ttcccaagta gagcggcggg ggggaattgc gaccaactcg tgcgcgtctt ctgcnccgcg 240

gcgggagccg gcgctgcgcg aacggctctc ctgcagctc atgctgcctg ccctgcgcct 300

getcagcctc gggtagcca cctccggagg gaccggggag cgcggcagcg ccgcggactc 360

ggcgtgctct cctccgggga cgcgggacga agaggcagcc ccggggcgcg cgcgggaggc 420

atg gag cgc tgc ccc agc ctg ggg gtc acc ctc tac gcc ctg gtg gtg 468
Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val
  1           5           10          15

gtc ctg ggg ctg cgg gca gca cca gcc ggc ggc cag cac tat cta cac 516
Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His
          20          25          30

atc cgc cca gca ccc agc gac aac ctg ccc ttg gtg gac ctc atc gaa 564
Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
          35          40          45

cat cca gac cct atc ttt gac cct aag gag aag gat ctg aac gag acg 612
His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
          50          55          60

ctg ctg cgc tcg ctg ctc ggg ggc cac tac gac ccg ggc ttt atg gcc 660
Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
          65          70          75          80

act tcg ccc cca gag gac cga ccc gga ggg ggc ggg gga ccg gct gga 708
Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Pro Ala Gly
          85          90          95

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Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His
 20 25 30
 Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
 35 40 45
 His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
 50 55 60
 Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
 65 70 75 80
 Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Pro Ala Gly
 85 90 95
 Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
 100 105 110
 Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
 115 120 125
 Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
 130 135 140
 Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
 145 150 155 160
 Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
 165 170 175
 Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
 180 185 190
 Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
 195 200 205
 Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
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 Ile Ser Glu Cys Lys Cys Ser Cys
 225 230

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26

<210> 14

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<220>

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<223> n=a, c, g, or t

<220>

<221> modified_base

<222> (15)

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<400> 14

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17

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<210> 18

<211> 18

<212> DNA

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<223> Description of Artificial Sequence:oligonucleotide

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<210> 19

<211> 6

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<213> mouse

<400> 19

Gln Met Trp Leu Trp Ser

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5

<210> 20

<211> 18

<212> DNA

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<223> Description of Artificial Sequence:oligonucleotide

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<210> 21

<211> 6

<212> PRT

<213> mouse

<400> 21

Glu Cys Lys Cys Ser Cys

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5

<210> 22

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